```
1    ATGAGCACGATTCCCAAACCTCAAAGAAAAACCAAACGTAACACCAAC
     MetSerThrIleProLysProGlnArgLysThrLysArgAsnThrAsn   16

49   CGTCGCCCACAGGACGTCAAGTTCCCGGGTGGCGGTCAGATCGTTGGT
     ArgArgProGlnAspValLysPheProGlyGlyGlyGlnIleValGly   32

97   GGAGTTTACTTGTTGCCGCGCAGGGGCCCTAGATTGGGTGTGCGCGCG
     GlyValTyrLeuLeuProArgArgGlyProArgLeuGlyValArgAla   48

145  ACGAGGAAGACTTCCGAGCGGTCGCAACCTCGAGGTAGACGTCAGCCT
     ThrArgLysThrSerGluArgSerGlnProArgGlyArgArgGlnPro   64

193  ATCCCCAAGGCACGTCGGCCCGAGGGCAGGACCTGGGCTCAGCCCGGG
     IleProLysAlaArgArgProGluGlyArgThrTrpAlaGlnProGly   80

241  TACCCTTGGCCCCTCTATGGCAATGAGGGTTGCGGGTGGGCGGGATGG
     TyrProTrpProLeuTyrGlyAsnGluGlyCysGlyTrpAlaGlyTrp   96

289  CTCCTGTCTCCCCGTGGCTCTCGGCCTAGCTGGGGCCCCACAGACCCC
     LeuLeuSerProArgGlySerArgProSerTrpGlyProThrAspPro  112

337  CGGCGTAGGTCGCGCAATTTGGGTAAGGTCATCGATACCCTTACGTGC
     ArgArgArgSerArgAsnLeuGlyLysValIleAspThrLeuThrCys  128

385  GGCTTCGCGCACCTCATGGGGTACATACCGCTCGTCGGCGCCCCTCTT
     GlyPheAlaHisLeuMetGlyTyrIleProLeuValGlyAlaProLeu  144

433  GGAGGCCGTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGAC
     GlyGlyArgAlaArgAlaLeuAlaHisGlyValArgValLeuGluAsp  160

481  GGCGTGAACTATGCAACAGGGAACCTTCCTGGTTGCTCTTTCTCTATC
     GlyValAsnTyrAlaThrGlyAsnLeuProGlyCysSerPheSerIle  176

529  TTCCTTCTGGCCCTGCTCTCTTGCCTGACTGTGCCCGCTTCAGCCTAC
     PheLeuLeuAlaLeuLeuSerCysLeuThrValProAlaSerAlaTyr  192

577  CAAGTGCGCAATTCCTCAGGGCTTTACCAGGTCACCAATGATTGCCCT
     GlnValArgAsnSerSerGlyLeuTyrGlnValThrAsnAspCysPro  208

625  AATTCGAGTATTGTGTACGAGGCGGCCGATGCCATCCTGCACACTCCG
     AsnSerSerIleValTyrGluAlaAlaAspAlaIleLeuHisThrPro  224

673  GGGTGTGTCCCTTGCGTTCGCGAGGGTAACGCCTCGAGGTGTTGGGTG
     GlyCysValProCysValArgGluGlyAsnAlaSerArgCysTrpVal  240

721  GCGGTGACCCCCACGGTGGCCACCAGGGACGGCAAACTCCCCACAACG
     AlaValThrProThrValAlaThrArgAspGlyLysLeuProThrThr  256

769  CAGCTTCGACGTCATATCGATCTGCTTGTCGGGAGCGCCACCCTCTGC
     GlnLeuArgArgHisIleAspLeuLeuValGlySerAlaThrLeuCys  272
```

FIGURE 9

```
817  TCGGCCCTCTACGTGGGGGACCTGTGCGGGTCTGTCTTTCTCGTTGGT
     SerAlaLeuTyrValGlyAspLeuCysGlySerValPheLeuValGly  288

865  CAACTGTTTACCTTCTCTCCCAGGCGCCACTGGACGACGCAAGACTGC
     GlnLeuPheThrPheSerProArgArgHisTrpThrThrGlnAspCys  304

913  AATTGTTCTATCTATCCCGGCCATATAACGGGTCATCGCATGGCATGG
     AsnCysSerIleTyrProGlyHisIleThrGlyHisArgMetAlaTrp  320

961  GATATGATGATGAACTGG
     AspMetMetMetAsnTrp                                326
```

FIGURE 9 (CONT.)

```
1    ATGTCCCCTATACTAGGTTATTGGAAAATTAAGGGCCTTGTGCAACCC
     MetSerProIleLeuGlyTyrTrpLysIleLysGlyLeuValGlnPro   16

49   ACTCGACTTCTTTTGGAATATCTTGAAGAAAAATATGAAGAGCATTTG
     ThrArgLeuLeuLeuGluTyrLeuGluGluLysTyrGluGluHisLeu   32

97   TATGAGCGCGATGAAGGTGATAAATGGCGAAACAAAAAGTTTGAATTG
     TyrGluArgAspGluGlyAspLysTrpArgAsnLysLysPheGluLeu   48

145  GGTTTGGAGTTTCCCAATCTTCCTTATTATATTGATGGTGATGTTAAA
     GlyLeuGluPheProAsnLeuProTyrTyrIleAspGlyAspValLys   64

193  TTAACACAGTCTATGGCCATCATACGTTATATAGCTGACAAGCACAAC
     LeuThrGlnSerMetAlaIleIleArgTyrIleAlaAspLysHisAsn   80

241  ATGTTGGGTGGTTGTCCAAAAGAGCGTGCAGAGATTTCAATGCTTGAA
     MetLeuGlyGlyCysProLysGluArgAlaGluIleSerMetLeuGlu   96

289  GGAGCGGTTTTGGATATTAGATACGGTGTTTCGAGAATTGCATATAGT
     GlyAlaValLeuAspIleArgTyrGlyValSerArgIleAlaTyrSer  112

337  AAAGACTTTGAAACTCTCAAAGTTGATTTTCTTAGCAAGCTACCTGAA
     LysAspPheGluThrLeuLysValAspPheLeuSerLysLeuProGlu  128

385  ATGCTGAAAATGTTCGAAGATCGTTTATGTCATAAAACATATTTAAAT
     MetLeuLysMetPheGluAspArgLeuCysHisLysThrTyrLeuAsn  144

433  GGTGATCATGTAACCCATCCTGACTTCATGTTGTATGACGCTCTTGAT
     GlyAspHisValThrHisProAspPheMetLeuTyrAspAlaLeuAsp  160

481  GTTGTTTTATACATGGACCCAATGTGCCTGGATGCGTTCCCAAAATTA
     ValValLeuTyrMetAspProMetCysLeuAspAlaPheProLysLeu  176

529  GTTTGTTTTAAAAAACGTATTGAAGCTATCCCACAAATTGATAAGTAC
     ValCysPheLysLysArgIleGluAlaIleProGlnIleAspLysTyr  192

577  TTGAAATCCAGCAAGTATATAGCATGGCCTTTGCAGGGCTGGCAAGCC
     LeuLysSerSerLysTyrIleAlaTrpProLeuGlnGlyTrpGlnAla  208

625  ACGTTTGGTGGTGGCGACCATCCTCCAAAATCGGATCTGATCGAAGGT
     ThrPheGlyGlyGlyAspHisProProLysSerAspLeuIleGluGly  224

673  CGTGGGATCCCCAATTCGAGCTCGGTACCCATGAGCACGATTCCCAAA
     ArgGlyIleProAsnSerSerSerValProMetSerThrIleProLys  240

721  CCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCCACAGGACGTC
     ProGlnArgLysThrLysArgAsnThrAsnArgArgProGlnAspVal  256

769  AAGTTCCCGGGTGGCGGTCAGATCGTTGGTGGAGTTTACTTGTTGCCG
     LysPheProGlyGlyGlyGlnIleValGlyGlyValTyrLeuLeuPro  272
```

FIGURE 10

```
817  CGCAGGGGCCCTAGATTGGGTGTGCGCGCGACGAGGAAGACTTCCGAG
     ArgArgGlyProArgLeuGlyValArgAlaThrArgLysThrSerGlu  288

865  CGGTCGCAACCTCGAGGTAGACGTCAGCCTATCCCCAAGGCACGTCGG
     ArgSerGlnProArgGlyArgArgGlnProIleProLysAlaArgArg  304

913  CCCGAGGGCAGGACGGGGATCGGGAATTCATCGTGA
     ProGluGlyArgThrGlyIleGlyAsnSerSerEnd              315
```

FIGURE 10 (CONT.)